IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

IN THE APPLICATION OF:
GLASSMAN ET AL.   CASE NO.: BB1449 US NA

APPLICATION NO.: UNKNOWN   GROUP ART UNIT: UNKNOWN

FILED: CONCURRENTLY HEREWITH   EXAMINER: UNKNOWN

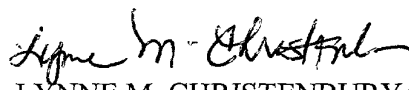FOR: **RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION**

Assistant Commissioner for Patents
Washington, DC 20231

Sir:

DECLARATION IN ACCORDANCE WITH 37 CFR 1.821

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 CFR 1.821(c) and (e), respectively are the same.

Respectfully submitted,

LYNNE M. CHRISTENBURY
ATTORNEY FOR APPLICANTS
REGISTRATION NO. 30,971
TELEPHONE: 302-992-5481
FACSIMILE: 302-892-1026

Dated: 22 June 2001

DECLARATION (37 CFR 1.63) FOR UTILITY OR DESIGN APPLICATION USING AN APPLICATION DATA SHEET (37 CFR 1.76)

As the below named inventor(s), I/we declare that:

This declaration is directed to:

☒ The attached application, docket BB1449 US NA or

☐ Application No. _____, filed on _____,

    ☐ as amended on _____ (if applicable);

I/we believe that I/we am/are the original and first inventor(s) of the subject matter which is claimed and for which a patent is sought;

I/ we have reviewed and understand the contents of the above-identified application, including the claims, as amended by any amendment specifically referred to above;

I/we acknowledge the duty to disclose to the United States Patent and Trademark Office all information known to me/us to be material to patentability as defined in 37 CFR 1.56, including material information which became available between the filing date of the prior application and the National or PCT International filing date of the continuation-in-part application, if applicable; and

All statements made herein of my/own knowledge are true, all statements made herein on information and belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like are punishable by fine or imprisonment, or both, under 18 U.S.C. 1001, and may jeopardize the validity of the application or any patent issuing thereon.

FULL NAME OF INVENTOR(S)

Inventor one: KIMBERLY F. GLASSMAN

Signature: _____   Citizen of: U.S.A.

Inventor two: WILLIAM J. GORDON-KAMM

Signature: _____   Citizen of: U.S.A.

Inventor three: ANTHONY J. KINNEY

Signature: _____   Citizen of: UNITED KINGDOM

Inventor four: KEITH S. LOWE

Signature: _____   Citizen of: U.S.A.

☐ Additional inventors are being named on 1 additional form(s) attached hereto.

FULL NAME OF INVENTOR(S)

Inventor one: SCOTT E. NICHOLS

Signature: _____   Citizen of: U.S.A.

Inventor two: KEVIN L. STECCA

Signature: _____   Citizen of: U.S.A.

Inventor three: _____

Signature: _____   Citizen of: _____

Inventor four: _____

Signature: _____   Citizen of: _____

SEQUENCE LISTING

<110> Glassman, Kimberly F.
      Gordon-Kamm, William J.
      Kinney, Anthony
      Lowe, Keith S.
      Nichols, Scott E.
      Stecca, Kevin L.

<120> RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION

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2

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<210>  10
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<212>  DNA
<213>  Artificial Sequence

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       of Cer3

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<210>  11
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<212>  DNA
<213>  Artificial Sequence

<220>
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gaattcgcgg ccgcggcacg agatttgagg                                    30


<210>  12
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<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence:  ELVISLIVES complementary
       region of pKS106 and pKS124

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cggccggagc tggtcatctc gctcatcgtc gagtcggcgg ccgccgactc gacgatgagc 60
gagatgacca gctccggccg                                               80


<210>  13
<211>  154
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<213>  Artificial Sequence
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3

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      region of pKS133

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<210> 14
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<213> Artificial Sequence

<220>
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<210> 15
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<212> DNA
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<220>
<223> Description of Artificial Sequence: ELVISLIVES PCR primer

<400> 15
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<210> 16
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer for amplification
       of soybean Fad2-1

<400> 16
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<210> 17
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer for amplification
       of soybean Fad2-1

<400> 17
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4

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<210>   18
<211>   32
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<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence:   PCR primer for amplification
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<400>   18
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<210>   19
<211>   32
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<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence:   PCR primer for amplification
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<210>   20
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<212>   DNA
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<220>
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        of soybean Fad2-1, 3'-end 75 nucleotide fragment

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<210>   21
<211>   32
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence:   PCR primer for amplification
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<400>   21
gaattcgcgg ccgctgagaa ataagggact aa                                   32


<210>   22
<211>   32
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<213>   Artificial Sequence
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<220>
<223>   Description of Artificial Sequence: PCR primer for amplification
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<400>   22
gaattcgcgg ccgcgagtgt gacgagaaga ga   32

<210>   23
<211>   22
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence: PCR primer for amplification
        of soybean Fad2-1, 3'-end 600 nucleotide fragment

<400>   23
gaattcgcgg ccgcttctga tgaatcgtaa tg   32

<210>   24
<211>   1717
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence: ELVISLIVES complementary
        region of pBS68

<400>   24
cggccggagc tggtcatctc gctcatcgtc gagtcggcgg ccgctgagtg attgctcacg   60
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6

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attaacctca attcttctaa g                                          21


<210>  26
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<210>  27
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<220>
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<400>  27
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<210>  28
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<220>
<223>  Description of Artificial Sequence:  PCR primer for amplification
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<400>  28
atccctgaag tgtctcattt ta                                         22


<210>  29
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<213>  Artificial Sequence
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7

<220>
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ccg   963

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<213> Glycine max

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8

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        35                  40                  45

Arg Lys Val Lys Ser Met Tyr Pro Leu Val Val Ala Val Leu Pro Asp
        50                  55                  60

Val Pro Gln Asp His Arg Asn Ile Leu Thr Ser Gln Gly Cys Ile Val
65                  70                  75                  80

Arg Glu Ile Glu Pro Val Tyr Pro Pro Glu Asn Gln Thr Gln Phe Ala
                85                  90                  95

Met Ala Tyr Tyr Val Ile Asn Tyr Ser Lys Leu Arg Ile Trp Glu Phe
            100                 105                 110

Val Glu Tyr Ser Lys Met Ile Tyr Leu Asp Gly Asp Ile Gln Val Phe
            115                 120                 125

Asp Asn Ile Asp His Leu Phe Asp Leu Pro Asp Asn Tyr Phe Tyr Ala
        130                 135                 140

Val Met Asp Cys Phe Cys Glu Pro Thr Trp Gly His Thr Lys Gln Tyr
145                 150                 155                 160

Gln Ile Gly Tyr Cys Gln Gln Cys Pro His Lys Val Gln Trp Pro Thr
                165                 170                 175

His Phe Gly Pro Lys Pro Pro Leu Tyr Phe Asn Ala Gly Met Phe Val
            180                 185                 190

Tyr Glu Pro Asn Leu Ala Thr Tyr Arg Asp Leu Leu Gln Thr Val Gln
            195                 200                 205

Val Thr Gln Pro Thr Ser Phe Ala Glu Gln Asp Phe Leu Asn Met Tyr
            210                 215                 220

Phe Lys Asp Lys Tyr Arg Pro Ile Pro Asn Val Tyr Asn Leu Val Leu
225                 230                 235                 240

Ala Met Leu Trp Arg His Pro Glu Asn Val Glu Leu Asp Lys Val Lys
                245                 250                 255

Val Val His Tyr Cys Ala Ala Gly Ser Lys Pro Trp Arg Tyr Thr Gly
            260                 265                 270

Lys Glu Glu Asn Met Glu Arg Glu Asp Ile Lys Met Leu Val Lys Lys
            275                 280                 285

Trp Trp Asp Ile Tyr Glu Asp Glu Thr Leu Asp Tyr Asn Asn Pro Leu
        290                 295                 300

Asn Val Asp Lys Phe Thr Ala Ala Leu Met Glu Val Gly Glu Val Lys
305                 310                 315                 320

Phe Val Arg Ala Pro Ser Ala Ala
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9

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ctaacatcac caccgttgtt gccaatgtca ccaccgagca attacccaag gctcgtggag    180
gaagtgggcg tgccttcgtg acctttcttg ctgggaacgg tgattacgta aagggtgtcg    240
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tcaattactc caagctacgt atttgggagt tcgtggagta caagaagacg atatacctag    480
acggtgacat ccaagtattt ggaaacatag accacttgtt tgatctgcct gataattatt    540
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ctgctgggtc taagccttgg aggttcactg ggaaggaaga gaacatggat agggaagata    960
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ttgtgccagc accttctgct gcctaatatg cttattattt acagctacaa attaatgtta   1140
attaacgaca aagtatatgt attgttattt gctttttttc gtttttgggt cttatatatg   1200
aaggaacaac gtctatggtt ttaatttgga tgaccttctt gtatacaaag ccacatgtga   1260
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<210> 33
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<212> PRT
<213> Glycine max

<400> 33
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            20                  25                  30

Ile Thr Thr Val Val Ala Asn Val Thr Thr Glu Gln Leu Pro Lys Ala
        35                  40                  45

Arg Gly Gly Ser Gly Arg Ala Phe Val Thr Phe Leu Ala Gly Asn Gly
    50                  55                  60

Asp Tyr Val Lys Gly Val Val Gly Leu Ala Lys Gly Leu Arg Lys Ala
65                  70                  75                  80

Lys Ser Met Tyr Pro Leu Val Val Ala Val Leu Pro Asp Val Pro Glu
                85                  90                  95

Glu His Arg Glu Ile Leu Lys Ser Gln Gly Cys Ile Val Arg Glu Ile
            100                 105                 110

Glu Pro Val Tyr Pro Pro Glu Asn Gln Thr Gln Phe Ala Met Ala Tyr
            115                 120                 125
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10

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Tyr Val Ile Asn Tyr Ser Lys Leu Arg Ile Trp Glu Phe Val Glu Tyr
    130             135             140

Lys Lys Thr Ile Tyr Leu Asp Gly Asp Ile Gln Val Phe Gly Asn Ile
145             150             155             160

Asp His Leu Phe Asp Leu Pro Asp Asn Tyr Phe Tyr Ala Val Met Asp
            165             170             175

Cys Phe Cys Glu Lys Thr Trp Ser His Thr Pro Gln Phe Gln Ile Gly
            180             185             190

Tyr Cys Gln Gln Cys Pro Asp Lys Val Gln Trp Pro Ser His Phe Gly
            195             200             205

Ser Lys Pro Pro Leu Tyr Phe Asn Ala Gly Met Phe Val Tyr Glu Pro
    210             215             220

Asn Leu Asp Thr Tyr Arg Asp Leu Leu Gln Thr Val Gln Leu Thr Lys
225             230             235             240

Pro Thr Ser Phe Ala Glu Gln Asp Phe Leu Asn Met Tyr Phe Lys Asp
            245             250             255

Lys Tyr Lys Pro Ile Pro Asn Met Tyr Asn Leu Val Leu Ala Met Leu
            260             265             270

Trp Arg His Pro Glu Asn Val Glu Leu Asp Lys Val Gln Val Val His
            275             280             285

Tyr Cys Ala Ala Gly Ser Lys Pro Trp Arg Phe Thr Gly Lys Glu Glu
    290             295             300

Asn Met Asp Arg Glu Asp Ile Lys Met Leu Val Lys Lys Trp Trp Asp
305             310             315             320

Ile Tyr Glu Asp Glu Thr Leu Asp Tyr Asn Asn Asn Ser Val Asn Val
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Glu Arg Phe Thr Ser Ala Leu Leu Asp Ala Gly Gly Phe Gln Phe Val
            340             345             350

Pro Ala Pro Ser Ala Ala
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<212>   DNA
<213>   Artificial Sequence

<220>
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        region of PHP17939

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agattgacgg ttgattgtat ttttgttttt tatggttttg tgttatgact taagtcttca  180
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11

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tctctttatc tcttcatcag gtttgacggt tacttaatat ggtgcatgca tgggtacatc  240
actagaaacc atggaaggta ccaagatatc aaccgcggaa agatcgtaca aatggcatgt  300
taaataaccg tcaaacctga tgaagagata aagagatgaa gacttaagtc ataacacaaa  360
accataaaaa acaaaaatac aatcaaccgt caatctgacc aatgcatgaa aaagctgcaa  420
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<210> 35
<211> 1968
<212> DNA
<213> Glycine max

<400> 35
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ctcaccaaac ccaaccacgc tctcaaaatc aaatgttcca tctccaaacc ccccacggcg  180
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gcgcgttcct ccggcctccc cggcgtctgc attgccacct ccggcccccgg cgccaccaac  480
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caggtcgccc gccggatgat cggcaccgac gccttccaag aaacccgat cgtggaggtg  600
agcagatcca tcacgaagca caactacctc atcctcgacg tcgacgacat ccccccgcgtc  660
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taccttcttg atgtcattgt gccccatcag gagcatgtgt tgccgatgat tcccagtaat 1920
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<210>   36
<211>   22
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence: PCR primer for amplification
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13